

**SCORE Search Results Details for Application 10573229 and
Search Result 20090528_121059_us-10-573-229a-1.rst.**

| Score Home | Retrieve Application | SCORE System | SCORE | Comments / Suggestions |
|----------------------------|--------------------------------------|------------------------------|-----------------------|--|
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GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 21:51:55 ; Search time 1876 Seconds
(without alignments)
47444.276 Million cell updates/sec

Title: US-10-573-229A-1

Perfect score: 920

Sequence: 1 tctgtataggggaaatggctg.....acccccaagaacacccctcta 920

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 83780570 seqs, 48372533981 residues

Total number of hits satisfying chosen parameters: 167561140

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

EST:*

1: qb est1:*

2: gb.est2:*

3: gb.est3:*

4: qb.est4:*

5: qb.est5:*

5: gb_est6:
6: gb_est6:*

7: qb_cscs:

```

9:  gb_est9:*
10:  gb_est10:*
11:  gb_est11:*
12:  gb_est12:*
13:  gb_est13:*
14:  gb_est14:*
15:  gb_est15:*
16:  gb_est16:*
17:  gb_est17:*
18:  gb_est18:*
19:  gb_gss1:*
20:  gb_gss2:*
21:  gb_gss3:*
22:  gb_gss4:*
23:  gb_gss5:*
24:  gb_gss6:*
25:  gb_gss7:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | Query | | | | | Description |
|--------|-------|-------|-------|--------|----|--------------------|
| | No. | Score | Match | Length | DB | |
| | 1 | 920 | 100.0 | 920 | 5 | BU183861 AGENCOURT |
| | 2 | 149.8 | 16.3 | 988 | 3 | BE733157 601567451 |
| | 3 | 108 | 11.7 | 533 | 10 | DB059978 DB059978 |
| c | 4 | 104.8 | 11.4 | 478 | 2 | AW269751 xv36g11.x |
| c | 5 | 104.8 | 11.4 | 484 | 2 | BE046932 hd92f06.x |
| | 6 | 104.4 | 11.3 | 500 | 10 | DB100179 DB100179 |
| c | 7 | 103.2 | 11.2 | 757 | 20 | CC492937 CH240_327 |
| | 8 | 101.4 | 11.0 | 526 | 10 | DB073121 DB073121 |
| | 9 | 101.2 | 11.0 | 669 | 22 | EI735387 CHORI5142 |
| c | 10 | 101.2 | 11.0 | 702 | 4 | BQ021722 UI-H-DH1- |
| | 11 | 95.4 | 10.4 | 549 | 10 | DB074846 DB074846 |
| c | 12 | 94.8 | 10.3 | 446 | 2 | AW297623 UI-H-BW0- |
| c | 13 | 94.6 | 10.3 | 533 | 1 | AA535137 nf87h12.s |
| | 14 | 94.6 | 10.3 | 637 | 2 | AW970418 EST382499 |
| c | 15 | 94.2 | 10.2 | 429 | 20 | CE539857 tigr-gss- |
| | 16 | 94 | 10.2 | 707 | 22 | EI399423 MUGQ_CH25 |
| | 17 | 94 | 10.2 | 805 | 22 | ED482970 MUGQ_CH25 |
| c | 18 | 92.8 | 10.1 | 381 | 25 | CU051182 Equus cab |
| c | 19 | 92.8 | 10.1 | 466 | 25 | CU288702 Equus cab |
| c | 20 | 92.4 | 10.0 | 548 | 10 | DB349144 DB349144 |
| c | 21 | 91.8 | 10.0 | 454 | 4 | BM667926 UI-E-DW0- |
| | 22 | 91.8 | 10.0 | 503 | 4 | BM696584 UI-E-DW0- |

| | | | | | | | |
|------|------|------|------|----|----------|----------|-------------|
| 23 | 91.8 | 10.0 | 1147 | 3 | BG119504 | BG119504 | 602349294 |
| 24 | 91.4 | 9.9 | 449 | 1 | AA426503 | AA426503 | zw02b10.r |
| c 25 | 91.4 | 9.9 | 682 | 6 | CA431350 | CA431350 | UI-H-FG1- |
| 26 | 91.4 | 9.9 | 688 | 5 | BX104512 | BX104512 | BX104512 |
| 27 | 91.4 | 9.9 | 830 | 3 | BG678891 | BG678891 | 602624794 |
| c 28 | 91 | 9.9 | 703 | 25 | CU177831 | CU177831 | Equus cab |
| c 29 | 90.8 | 9.9 | 284 | 3 | BF591952 | BF591952 | 7o22d02.x |
| c 30 | 90.8 | 9.9 | 365 | 3 | BF476176 | BF476176 | naa29d02. |
| c 31 | 90.8 | 9.9 | 421 | 1 | AI767873 | AI767873 | wi97h11.x |
| c 32 | 90.8 | 9.9 | 444 | 1 | AI218734 | AI218734 | oo07b06.x |
| c 33 | 90.8 | 9.9 | 448 | 3 | BF516187 | BF516187 | UI-H-BW1- |
| c 34 | 90.8 | 9.9 | 483 | 1 | AI697816 | AI697816 | AI697816 |
| c 35 | 90.8 | 9.9 | 493 | 1 | AI670048 | AI670048 | we17f06.x |
| c 36 | 90.8 | 9.9 | 508 | 1 | AI668692 | AI668692 | zb63a11.x |
| c 37 | 90.8 | 9.9 | 625 | 1 | AI990414 | AI990414 | wt74a11.x |
| c 38 | 90.8 | 9.9 | 629 | 5 | BU730892 | BU730892 | UI-E-CI1- |
| c 39 | 89 | 9.7 | 755 | 24 | AG621567 | AG621567 | Macaca fu |
| c 40 | 88.6 | 9.6 | 834 | 20 | CC062054 | CC062054 | MUGQ_CH25 |
| 41 | 88.4 | 9.6 | 496 | 25 | CU026287 | CU026287 | Equus cab |
| 42 | 87.6 | 9.5 | 457 | 10 | DB489743 | DB489743 | DB489743 |
| c 43 | 87.4 | 9.5 | 349 | 18 | M85416 | M85416 | EST01931 Fe |
| 44 | 87.4 | 9.5 | 760 | 24 | AG671147 | AG671147 | Macaca fu |
| c 45 | 87.2 | 9.5 | 739 | 25 | CT974461 | CT974461 | Equus cab |

ALIGNMENTS

RESULT 1

BU183861

| | | | | | | |
|------------|---|--------------|------------|---------------|-----|-------------|
| LOCUS | BU183861 | 920 bp | mRNA | linear | EST | 04-SEP-2002 |
| DEFINITION | AGENCOURT_7964945 NIH_MGC_72 | Homo sapiens | cDNA clone | IMAGE:6162433 | | |
| | AGENCODE sequence. | | | | | |
| ACCESSION | BU183861 | | | | | |
| VERSION | BU183861.1 | GI:22697845 | | | | |
| KEYWORDS | EST. | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; | | | | | |
| | Catarrhini; Hominidae; Homo. | | | | | |
| REFERENCE | 1 (bases 1 to 920) | | | | | |
| AUTHORS | NIH-MGC http://mgc.nci.nih.gov/ . | | | | | |
| TITLE | National Institutes of Health, Mammalian Gene Collection (MGC) | | | | | |
| JOURNAL | Unpublished (1999) | | | | | |
| COMMENT | Contact: Robert Strausberg, Ph.D. | | | | | |
| | Email: cgapbs-r@mail.nih.gov | | | | | |
| | Tissue Procurement: ATCC/DCTD/DTP | | | | | |
| | CDNA Library Preparation: Life Technologies, Inc. | | | | | |

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13516 row: f column: 02
High quality sequence stop: 633.

FEATURES Location/Qualifiers
source 1. .920
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6162433"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_72"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN

```

Query Match          100.0%; Score 920; DB 5; Length 920;
Best Local Similarity 100.0%; Pred. No. 1.6e-249;
Matches 920; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 TCTGTAGAGGGGAATGGCTGCTGTCAATGGGGTGACAGCCCAGTGGAGAGGTG 60
|||||

Qy 61 CACTTGGTGAGAAACCGATGCCCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGAC 120

Qy 121 TGAGGCCACTTGGAAAGCTGATCTGGAGCACCGTAGCAGCCCTAGCTGGCTGAGCCAC 180

Db 121 TGAGCCACTTGGAAAGCTGATCTTGGAGCACCGTCAGGCCCTAGCTGGCTGCAGCCAC 180

Db 181 AGCCAAACAAGACTGCAACCTCTGGGGATCCTGAGCCAGAATCCCCGGCTAAATT 240

Db 241 GCTCCTGATTCTAACCCACAGAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAA 300

QY 301 GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGTGTGCCAATGCAGGAATGCTGGCC 360
DQ 301 GATCCCAGTAGGGCAGGAGACAGGAGCACCTCTGTGTGCCAATGCAGGAATGCTGGCC 360

Qy 361 ATCATTGCTTGTGGCGACTGAGAACATCACCCACTCCCCAGAACCTTTTACG 420
|||
Db 361 ATCATTGCTTGTGGCGACTGAGAACATCACCCACTCCCCAGAACCTTTTACG 420

Qy 421 TGGAGTAAAATTAAAGGGCTGTCCAGCTAACCTCAAACCTCCAGATCCCAGTC 480
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Db 421 TGGAGTAAAATTAAAGGGCTGTCCAGCTAACCTCAAACCTCCAGATCCCAGTC 480

Qy 481 TTCTCTGCTTGTCAAAAGGACTCAAGTGAAAGACATCTGCAGCTGTGAACGGGTA 540
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Db 481 TTCTCTGCTTGTCAAAAGGACTCAAGTGAAAGACATCTGCAGCTGTGAACGGGTA 540

Qy 541 AAACCCCTGCCAGGGCCAAAGCAAGGATTCCCTAGCGGGGAGGAAGGTAGAATC 600
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Db 541 AAACCCCTGCCAGGGCCAAAGCAAGGATTCCCTAGCGGGGAGGAAGGTAGAATC 600

Qy 601 GAGAGACCTCTAACCTGGAGAGGGAGGGAAATCCGAGGACCAGGGTTATGCA 660
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Db 601 GAGAGACCTCTAACCTGGAGAGGGAGGGAAATCCGAGGACCAGGGTTATGCA 660

Qy 661 CAACACAAGGGAAAGTACCTGCTGGTTCTGGGGTTGGGGAAAGGAAATCCCTACTGCC 720
|||
Db 661 CAACACAAGGGAAAGTACCTGCTGGTTCTGGGGTTGGGGAAAGGAAATCCCTACTGCC 720

Qy 721 CAAGAGCCAGCCCCGAACCCAAGGCACAGCTATACTGGCCCCGGGCCTGGGGGGCAC 780
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Db 721 CAAGAGCCAGCCCCGAACCCAAGGCACAGCTATACTGGCCCCGGGCCTGGGGGGCAC 780

Qy 781 GAAAACCTGAAAAAGGGCGCCTCCCAGCTCCCCGGGGTAAGGGCTTACCCCCCA 840
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Db 781 GAAAACCTGAAAAAGGGCGCCTCCCAGCTCCCCGGGGTAAGGGCTTACCCCCCA 840

Qy 841 GAGGGGGGGGGAAAAATCGAGTGGGATTTCCCAACCGCCGAAGACTAAACCTTAA 900
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Db 841 GAGGGGGGGGGAAAAATCGAGTGGGATTTCCCAACCGCCGAAGACTAAACCTTAA 900

Qy 901 ACCCCCCAAAGAAACCTTCTA 920
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Db 901 ACCCCCCAAAGAAACCTTCTA 920

RESULT 2

BE733157

LOCUS BE733157 988 bp mRNA linear EST 15-SEP-2000
DEFINITION 601567451F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3842292 5',
mRNA sequence.
ACCESSION BE733157
VERSION BE733157.1 GI:10147149

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 988)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM535 row: e column: 13
High quality sequence stop: 703.
FEATURES Location/Qualifiers
source 1 .988
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3842292"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Db 61 CAACAAGACTGCAACCTCCTGGGGATCTGAGCCAGAATCCCCTGGCTAAATTGCTCCT 120
 Qy 247 TGATTCTTAACCCACAGAAAATTGTGTAAGACCTCCATCAGGTGTCGACAAGGAAGAT 303
 ||||||||||||||||||||||| || | ||| | | ||||| |||
 Db 121 TGATTCTTAACCCACAGAAAATTGTGCTAACACCATGCAGAAGCTGCCAAGGCTTAT 177

RESULT 3

DB059978

LOCUS DB059978 533 bp mRNA linear EST 18-JAN-2008
 DEFINITION DB059978 TESTI2 Homo sapiens cDNA clone TESTI2053144 5', mRNA sequence.
 ACCESSION DB059978
 VERSION DB059978.1 GI:83532935
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 533)
 AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
 TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
 JOURNAL Genome Res. 16 (1), 55-65 (2006)
 PUBMED 16344560
 COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.
 FEATURES Location/Qualifiers
 source 1..533
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="TESTI2053144"

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/tissue_type="testis"
/clone_lib="TESTI2"
/note="Vector: pME18SFL3"
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ORIGIN

Query Match 11.7%; Score 108; DB 10; Length 533;
 Best Local Similarity 67.5%; Pred. No. 8.3e-19;
 Matches 181; Conservative 0; Mismatches 85; Indels 2; Gaps 2;

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|----|--|
| Qy | 9 GGGGAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGT 68 |
| | |
| Db | 22 GGGAAAGCAGCTACCATGTTGAGGCTGCTCAAGTAGCCTGTGGAGAGGTCCACCTGG 81 |
| Qy | 69 GAGAAACCGATGCCCTGCCAACCACCTGCACTAACCTGCTGGGCTGAGACTGAGCCAC 128 |
| | |
| Db | 82 GAGAAAACAAGGCCTTGCC-ACAGCCGGCACCAACTGCCAACCATCTGAGTCAGCCAC 140 |
| Qy | 129 TTGGAAGCTGATCTTGGAGCACCAGTCAGCCCTAGCTGGCTGCAGCCACAGCCAACA 188 |
| | |
| Db | 141 CTGGAAAGTGGATCCTCCAGCCTCATTCCAGCCTCAGATGACCACTGTCCCAGCTCAT 200 |
| Qy | 189 ACAAGACTGCAACCTCTGGGGATCTGAGCCAGAATCCCCTGGCTAAATTGCTCCTG 248 |
| | |
| Db | 201 TCTAGACTGCAACCTCATGAGAGACCTGGAGCCAGAA-CACCCAGCTAACGCTGTTCTGA 259 |
| Qy | 249 ATTCTTAACCCACAGAAAATTTGTAAGA 276 |
| | |
| Db | 260 ATTCCCGACTCACAGAGACTATGAAAGA 287 |

RESULT 4

AW269751/c

LOCUS AW269751 478 bp mRNA linear EST 03-JAN-2000
 DEFINITION xv36g11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2815268 3', mRNA sequence.
 ACCESSION AW269751
 VERSION AW269751.1 GI:6656781
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 478)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free from the IMAGE Consortium (info@image.llnl.gov).
Seq primer: -40UP from Gibco
High quality sequence stop: 446

FEATURES

Location/Qualifiers
1. .478
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2815268"
/lab_host="DH10B"
/clone_lib="#Soares_NFL_1"
/note="Organ: pooled; Ve-
Site_2: Eco RI; Equal am-
normalized libraries (fe-
B-cell NCI_CGAP_GCB1) we-
in vitro. Following HAP-
tracer in a subtractive
was PCR-amplified cDNAs
from the same 3 libraries
I.M.A.G.E. clones 297480,
726408-728711, and 72905.
Soares and M. Fatima Bon-

ORIGIN

RESULT 5

BE046932/c

LOCUS BE046932 484 bp mRNA linear EST 08-JUN-2000

DEFINITION hd92f06.x2 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2916995 3', mRNA sequence.

ACCESSION BE046932

VERSION BE046932.1 GI:8363985

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 484)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 476.

FEATURES Location/Qualifiers

source 1..484

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2916995"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_GC6"
/note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and

1475592-1476743). Subtraction by Bento Soares and M. Fatima Ronaldo."

ORTGDN

RESULT 6

DB100179

LOCUS DB100179 500 bp mRNA linear EST 18-JAN-2008
DEFINITION DB100179 TESTI4 Homo sapiens cDNA clone TESTI4052031 5', mRNA sequence.
ACCESSION DB100179
VERSION DB100179.1 GI:83431172
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 500)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T.,
Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H.,
Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N.,
Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M.,
Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A.,
Tanase,T., Naqai,K., Kikuchi,H., Nakai,K., Isoqai,T. and Sugano,S.

TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes

JOURNAL Genome Res. 16 (1), 55-65 (2006)

PUBMED 16344560

COMMENT Contact: Takao Isogai
 FLJ Project (HRI Team)
 Helix Research Institute
 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
 Email: flj-cdna@nifty.com
 NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

FEATURES Location/Qualifiers

source

- 1. .500
- /organism="Homo sapiens"
- /mol_type="mRNA"
- /db_xref="taxon:9606"
- /clone="TESTI4052031"
- /tissue_type="testis"
- /clone_lib="TESTI4"
- /note="Vector: pME18SFL3"

ORIGIN

Query Match 11.3%; Score 104.4; DB 10; Length 500;
 Best Local Similarity 67.8%; Pred. No. 8.6e-18;
 Matches 175; Conservative 0; Mismatches 81; Indels 2; Gaps 2;

| | | | |
|----|-----|--|-----|
| Qy | 19 | TGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACCGA | 78 |
| | | | |
| Db | 1 | TACCATGTTGTGAGGCTGCTCAAGTAGCCTTGTGGAGAGGTCCACCTGGAGAGAAAACAA | 60 |
| Qy | 79 | TGCCCTCTGCCAACCACCTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTGGAAAGCT | 138 |
| | | | |
| Db | 61 | GGCCTTGGC-ACAGCGGCACCAACTGCCAACCATCTGAGTCAGCCACCTGGAAAGTG | 119 |
| Qy | 139 | GATCTTGGAGCACCACTGCAAGCCCCTAGCTGGCTGCAGCCACAGCCAACAACAAAGACTGC | 198 |
| | | | |
| Db | 120 | GATCCTCCAGCCTCATTCAGCCTTCAGATGACCACTGTCAGCTCATATCTAGACTGC | 179 |
| Qy | 199 | AACCTCCTGGGGATCCTGAGCCAGAACTCCCTGGCTAAATTGCTCTTGATTCTAAC | 258 |
| | | | |
| Db | 180 | AACCTCATGAGAGACCTGGAGCCAGAA-CACCCAGCTAGCTGTTCTGAATTCCCGACT | 238 |
| Qy | 259 | CACAGAAATTGTGTAAGA | 276 |
| | | | |

Db 239 CACAGAGACTATGAAAGA 256

RESULT 7
 CC492937/c

LOCUS CC492937 757 bp DNA linear GSS 17-JUN-2003

DEFINITION CH240_327A8.T7 CHORI-240 Bos taurus genomic clone CH240_327A8, genomic survey sequence.

ACCESSION CC492937

VERSION CC492937.1 GI:31803851

KEYWORDS GSS.

SOURCE Bos taurus (cattle)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 757)

AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L., Tsai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M., Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R., Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S., Schein,J., Marra,M., de Jong,P., McWilliam,S., Barris,W., Dalrymple,B.P. and Tellam,R.

TITLE Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

JOURNAL Unpublished (2003)

COMMENT Other_GSSs: CH240_327A8.TARBAC13P2
 Contact: Rob Holt
 Sequencing
 The British Columbia Cancer Agency Genome Science Centre
 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
 Tel: 604-877-6085
 Fax: 604-877-6276
 Email: rholt@bcgsc.ca
 Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/ordering_information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.
 Plate: 327 row: A column: 8
 Seq primer: T7
 Class: BAC ends.

FEATURES Location/Qualifiers

source 1..757
 /organism="Bos taurus"
 /mol_type="genomic DNA"
 /strain="breed: Hereford"

```
/db_xref="taxon:9913"
/clone="CH240_327A8"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
```

ORIGIN

| | | | | | | | | | |
|-----------------------|-------|---|----------|------------|-----|--------|------|------|----|
| Query Match | 11.2% | Score | 103.2; | DB | 20; | Length | 757; | | |
| Best Local Similarity | 64.1% | Pred. No. | 2.1e-17; | | | | | | |
| Matches | 173; | Conservative | 0; | Mismatches | 93; | Indels | 4; | Gaps | 1; |
| Qy | 2 | CTGTAGAGGGAAATGGCTGCTGTGCATGGGGTCATGAGCAGCCCAGTGGAGAGGTGC | 61 | | | | | | |
| Db | 612 | CTCTGGGAAGTTGGCTGCATTCTATGAGGACATTACATGCCCTATGGAGATATCT | 553 | | | | | | |
| Qy | 62 | ACTTGGTGAGAACCGATGCCTCTGCCAACACCACCTGCACAAACCTGCTGGGTCTGAGACT | 121 | | | | | | |
| Db | 552 | GTGTGGTGAGGAACCTGAGGCTGTTGACAACACCCAGCACTATCTTCTGGGTGTGAAT | 493 | | | | | | |
| Qy | 122 | GAGCCAC----TTTGGAAAGCTGATCTGGAGCACCAAGTCAAGCCCTAGCTGGCTGCAGC | 177 | | | | | | |
| Db | 492 | GAATGACCAAATTGGAAAGAAAATCTCCAGCCTCAGTCAGGCCTCAGGTGACTGTAGC | 433 | | | | | | |
| Qy | 178 | CACAGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGGCCAGAATCCCTGGCTAA | 237 | | | | | | |
| Db | 432 | CGCAGCCAACATCTAGACTGCAACCTCCTGAGAGACTCTGAACCATAACCACCCAAC TAA | 373 | | | | | | |
| Qy | 238 | ATTGCTCTTGATTCTAACCCACAGAAAT | 267 | | | | | | |
| Db | 372 | GTTGTCCCCGAATTCTGACCCATGAAAGT | 343 | | | | | | |

RESULT 8

DB073121

LOCUS DB073121 526 bp mRNA linear EST 18-JAN-2008
DEFINITION DB073121 TESTI4 Homo sapiens cDNA clone TESTI4016394 5', mRNA sequence.
ACCESSION DB073121
VERSION DB073121.1 GI:83564345
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 526)

RESULT 9

EI735387

Locus EI735387 669 bp DNA linear GSS 28-OCT-2007
Definition CHORI514_21_012TR BAC library from the primary breast tumor sample s104 Homo sapiens genomic clone CHORI514_21_012, genomic survey sequence.
Accession EI735387
Version EI735387.1 GI:158756676
Keywords GSS.
Source Homo sapiens (human)
Organism Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
Reference 1 (bases 1 to 669)
Authors Raphael,B.J., Volik,S.V., Yu,P., Wu,C., Huang,G.Q., Waldman,F.,
Costello,J., Pienta,K., Mills,G., Bajsarowicz,K., Kobayashi,Y.,
Sridharan,S., Paris,P., Tao,Q.Z., Gray,J.W., Cheng,J.F., de
Jong,P., Nefedov,M., Aerni,S., Brown,R.P., Bashir,A.,
Padilla-Nash,H.M. and Collins,C.C.
Title A sequence-based survey of the complex structural organization of tumor genomes
Journal Unpublished (2007)
Comment Contact: Volik SV
Colin Collins' lab
UCSF Department of Urology
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7067
Fax: 415 476 8218
Email: svolik@cc.ucsf.edu
Seq primer: KBR/TJ 5'CTGGCCGTCGACATTAGG-3'.
Features Location/Qualifiers
source 1. .669
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="CHORI514_21_012"
 /tissue_type="Primary tumor"
 /clone_lib="BAC library from the primary breast tumor sample s104"

/note="Organ: Breast; Vector: pBACGK1.1; Site_1: HindIII;
 This library was constructed from s104 primary breast
 tumor sample by Dr. M. Nefedov (Dr. Peter de Jong's
 laboratory). The patient did not receive chemo- or
 radiotherapy and did not have recurrence for 10 years
 after surgery."

ORIGIN

| | | | | | | | | | |
|-----------------------|-------|--|---------|------------|----|--------|-----|------|---|
| Query Match | 11.0% | Score | 101.2 | DB | 22 | Length | 669 | | |
| Best Local Similarity | 62.8% | Pred. No. | 7.6e-17 | | | | | | |
| Matches | 157 | Conservative | 0 | Mismatches | 93 | Indels | 0 | Gaps | 0 |
| Qy | 18 | CTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGGGTGCACTGGTGAGAACCG | 77 | | | | | | |
| | | | | | | | | | |
| Db | 130 | CTGCCATGTCGTGAGAACACACAAGCAGCCCCAAGGAGGGTCCGTGTTGAAGGAAC | 189 | | | | | | |
| Qy | 78 | ATGCCTCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGACTGAGGCCACTTGGAA | 137 | | | | | | |
| | | | | | | | | | |
| Db | 190 | AGACCCCTGCTGGCAGCCAACACCACATTGCCAACATTGTGAGTGACCCATCTGGAC | 249 | | | | | | |
| Qy | 138 | TGATCTTGGAGCACCACTGCAAGCCCTAGCTGGCTGCAGCCACAGCCAACAACAAG | 197 | | | | | | |
| | | | | | | | | | |
| Db | 250 | AGGTTCCCTGACATCCTGTGAAGCCTCAGCTGACTGCAGCCCTGCTGACATCTGACT | 309 | | | | | | |
| Qy | 198 | CAACCTCTGGGGATCCTGAGCCAGAACATCCCTGGCTAAATTGCTCCTGATTCTAAC | 257 | | | | | | |
| | | | | | | | | | |
| Db | 310 | CAACCTCATGAGAGATCCAAACAAGAACTACCCAGCTAAGCCATTCCCTGATTCTGAT | 369 | | | | | | |
| Qy | 258 | CCACAGAAAT | 267 | | | | | | |
| | | | | | | | | | |
| Db | 370 | CCACAGAAAT | 379 | | | | | | |

RESULT 10

BQ021722/c

| | | | | | | |
|------------|---|---|----------------|------------|-----|-------------|
| LOCUS | BQ021722 | 702 bp | mRNA | linear | EST | 27-MAR-2002 |
| DEFINITION | UI-H-DH1-axi-n-10-0-UI.s1 | NCI_CGAP_DH1 | Homo sapiens | cDNA clone | | |
| | IMAGE:5829321 | 3' | mRNA sequence. | | | |
| ACCESSION | BQ021722 | | | | | |
| VERSION | BQ021722.1 | GI: | 19757000 | | | |
| KEYWORDS | EST. | | | | | |
| SOURCE | Homo sapiens (human) | | | | | |
| ORGANISM | Homo sapiens | | | | | |
| | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | | |
| | Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; | | | | | |
| | Catarrhini; Hominidae; Homo. | | | | | |
| REFERENCE | 1 | (bases 1 to 702) | | | | |
| AUTHORS | NCI-CGAP | http://www.ncbi.nlm.nih.gov/ncicgap . | | | | |
| TITLE | National Cancer Institute, Cancer Genome Anatomy Project (CGAP), | | | | | |

Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

The following repetitive elements were found in this cDNA

sequence: 16-517, >MLT1F#LTR/MaLR (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

| | |
|--------|---|
| source | Location/Qualifiers |
| | 1. .702 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:5829321" /tissue_type="Metastatic Chondrosarcoma" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI_CGAP_DH1" /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_DH1 is a normalized cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AGATCATTCG." TAG_TISSUE=lung TAG_LIB=UI-H-DH1 TAG_SEQ=AGATCATTCG" |

ORIGIN

Query Match 11.0%; Score 101.2; DB 4; Length 702;

Best Local Similarity 62.8%; Pred. No. 7.7e-17;

Matches 157; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

| | |
|----|---|
| Qy | 18 CTGCTGTGTCATGGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTGGTGAGAAACCG 77 |
| | |

RESULT 11

DB074846

LOCUS DB074846 549 bp mRNA linear EST 18-JAN-2008
DEFINITION DB074846 TESTI4 Homo sapiens cDNA clone TESTI4018555 5', mRNA sequence.
ACCESSION DB074846
VERSION DB074846.1 GI:83099624
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 549)
AUTHORS Kimura,K., Wakamatsu,A., Suzuki,Y., Ota,T., Nishikawa,T., Yamashita,R., Yamamoto,J., Sekine,M., Tsuritani,K., Wakaguri,H., Ishii,S., Sugiyama,T., Saito,K., Isono,Y., Irie,R., Kushida,N., Yoneyama,T., Otsuka,R., Kanda,K., Yokoi,T., Kondo,H., Wagatsuma,M., Murakawa,K., Ishida,S., Ishibashi,T., Takahashi-Fujii,A., Tanase,T., Nagai,K., Kikuchi,H., Nakai,K., Isogai,T. and Sugano,S.
TITLE Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes
JOURNAL Genome Res. 16 (1), 55-65 (2006)
PUBMED 16344560
COMMENT Contact: Takao Isogai
FLJ Project (HRI Team)
Helix Research Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Email: flj-cdna@nifty.com

NEDO human cDNA project (New Energy and Industrial Technology Developmental Organization, Japan); cDNA library construction: Helix Research Institute (HRI); 5'-end one pass sequencing: HRI, Research Association for Biotechnology (RAB) and Biotechnology Center, National Institute of Technology and Evaluation; 3'-end one pass sequencing: RAB.

| FEATURES | Location/Qualifiers |
|----------|--|
| source | 1. .549 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="TESTI4018555" /tissue_type="testis" /clone_lib="TESTI4" /note="Vector: pME18SFL3" |

ORIGIN

Query Match 10.4%; Score 95.4; DB 10; Length 549;
Best Local Similarity 63.1%; Pred. No. 3.2e-15;
Matches 171; Conservative 0; Mismatches 86; Indels 14; Gaps 1;

Qy 17 GCTGCTGTGTCATGGGGTGCATGAGCAGCCCAGTGGAGAGGTGCACTTGGTGAGAAACC 76

7 GCTGCCCTGTCA TGACGGTATGCATGGAGCCCCATGGAGAGGCCCATGATGAGGA 66

Qy 77 GATGCCTCTGCCAACCAACCTGCACTAACCTGCTGGGCTGAGACTGAGCCACTTGGAAAG 136

CCGAAAGCACTAAGTCCGTGCTCTTTGATACGGGACTTTGGACC 113

Qy 137 CTGATCTGGAGCACAGTCAGCCCTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196

Db 113 CAGATTCTCCAGCCTTGGTCAGGCCTTCAGATGACTGCAGCCTGGCTGTGACTTGACT 172

Db 173 GCCACCTCATGAGAGACCTTGAGCCAGAACCAAGCCACTCCTGGATTCTGA 232

Qy 257 CCCACAGAAATTGTGTAAGACCTCCATCAGG 287

100 200 300 400 500 600 700 800 900

RESULT 13

AN397623/a

LOCUS AW297623 C 446 bp mRNA linear EST 16-JAN-2000

DEFINITION UI-H-BW0-ajg-f-08-0-UI.s1 NCI_CGAP_Sub6 Homo sapiens cDNA clone
EMBL: G731010_31 rRNA precursor

IMAGE:27

ACCESSION # AW297623

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 446)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html The following repetitive elements were found in this cDNA sequence: 49-424, >MLT1F#LTR/MaLR Seq primer: M13 Forward
POLYA=Yes.

FEATURES Location/Qualifiers

source 1..446
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2731910"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI_CGAP_Sub6"
 /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub6 is a subtracted library derived from BW, which consists of a mixture of four normalized libraries: NCI_CGAP_Brn50, NCI_CGAP_Lu13, NCI_CGAP_Ov18, GBC1. The NCI_CGAP_Sub6 library had 7 million recombinants. A single-stranded DNA preparation of BW was used as a tracer in a subtractive hybridization with a driver comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855); NCI_CGAP_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743); NCI_CGAP_Pr22 pool 1 LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759,

1101192-1101959, 1217928-1220615); NCI_CGAP_Co10 pool 1
LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs
1057416-1061255, 1144584-1145351). (50% of the driver
population), plus a pool of 3,840 arrayed clones from
NCI_CGAP_Sub1 (IMAGE CloneIDs 2708616-2710535) and
NCI_CGAP_Sub2 (IMAGE CloneIDs 2710536-2712455) (20% of
the driver population), plus a pool of 11,136 clones from
NCI_CGAP_Sub3 (IMAGE CloneIDs 2712456-2723591) (30% of
the driver population). Subtraction was performed as
previously described [Bonaldo, Lennon & Soares (1996):
Normalization and Subtraction: Two Approaches To
Facilitate Gene Discovery. Genome Research 6, 791-806.
TAG_TISSUE=B cells germinal
TAG_LIB=Gbc1
TAG_SEQ=TCA"

ORIGIN

Query Match 10.3%; Score 94.8; DB 2; Length 446;
Best Local Similarity 67.1%; Pred. No. 4.5e-15;
Matches 149; Conservative 0; Mismatches 72; Indels 1; Gaps 1;

Qy 47 CCAGTGGAGAGGTGCACTTGGTGAGAAACCGATG-CCTCTGCCAACCACCTGCACTAAC 105

Pb 328 CCTATGGAGATGCCCATGTGGGAAGAATGGAGTCCCCCTGCCAACATGAGTTGACA 269

Qy 106 TGCTGGTCTGAGACTGAGCCACTTGGAAAGCTGATCTGGAGCACCAAGTCAGGCCCTTA 165

Pb 368 TCCGAACCGTCTGAGCCGACGGATGTGCAAAACGGACTGTTGCACCCCCAATGACCCGTTCA 398

Qy 166 GCTGGCTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAA 225

Pb 398 GATGACTCCAGCCCTCGCCACCTCGCTGACTCCGACCTGATTCGAGACGCCGAGCA 149

Qy 226 TCCCCCTGGCTAAATTGCTCCTTGATTCTAACCCACAGAAAT 267

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

RESULT 13

RESUME 13

AA535137/C 522-hc EPD# 11-000000 EST 01 AUG 1997

DEFINITION nf87h12.s1 NCI_CGAP_Co3 Homo sapiens cDNA clone IMAGE:926951 3',
LOCUS AA553513.7 533 bp mRNA linear EST ZI-AUG-1

mRNA seq

ACCESSION AA535137

VERSION AA53

KEYWORDS EST.

SOURCE *Homo sapiens*

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 533)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 826 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 440.

FEATURES Location/Qualifiers

source

- 1. .533
- /organism="Homo sapiens"
- /mol_type="mRNA"
- /db_xref="taxon:9606"
- /clone="IMAGE:926951"
- /sex="pooled"
- /tissue_type="colon"
- /lab_host="DH10B"
- /clone_lib="NCI_CGAP_Co3"
- /note="Vector: pT7T3D-PacI; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization."

ORIGIN

| | | | | | | | | | |
|-----------------------|-------|--------------|---------|------------|----|--------|-----|------|---|
| Query Match | 10.3% | Score | 94.6 | DB | 1 | Length | 533 | | |
| Best Local Similarity | 62.3% | Pred. No. | 5.3e-15 | | | | | | |
| Matches | 175 | Conservative | 0 | Mismatches | 89 | Indels | 17 | Gaps | 1 |

Qy 8 AGGGGAATGGCTGCTGTGTCATGGGGTGATGAGCAGCCCAGTGGAGAGGTGCACCTGG 67
 ||||| || | ||||| ||||| | ||||||| ||||| || | || |||

Db 478 AGGGAGAAGTCAGCTGTCATGCGAGGGCACTCAAGCAGCCCTGTGGAAAGCTCTACGTGG 419

Qy 68 TGAGAACCGATGCCCTGCCAACCACCTGCACTAACCT-----GCTG 110
 ||||||| || | ||||| | | ||||| || | || ||

Db 418 TGAGAAACTGAAGCCTCTGCCAACACCAACAAGGAACGTGAGACCTACTTCAAACAGCCA 359
 Qy 111 GGTCTGAGACTGAGCCACTTGGAGCTGATCTGGAGCACCGAGTCAGGCCCTAGCTGG 170
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 358 TCTGAGTGATCGATCCATCTGGAACAGATCCTCCAGGCCAGTCAGTCTCAGATGA 299
 Qy 171 CTGCAGCCACAGCCAACAACAAGACTGCAACCTCCTGGGGATCCTGAGCCAGAATCCCC 230
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 298 CTGCAGCCCTGACCAGCATCTCAACTGCAACCTCGTGAATGACCCGAGCCAGAACATG 239
 Qy 231 TGGCTAAATTGCTCCTGATCTTAACCCACAGAAAATTGTG 271
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 238 CAACTAAACTCTGCGTGGATTGATGACCCACAGAAAATTGTG 198

RESULT 14

AW970418

LOCUS AW970418 637 bp mRNA linear EST 01-JUN-2000
 DEFINITION EST382499 MAGE resequences, MAGK Homo sapiens cDNA, mRNA sequence.
 ACCESSION AW970418
 VERSION AW970418.1 GI:8160263
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 637)
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
 Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 TITLE Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray
 JOURNAL Unpublished (2000)
 COMMENT Contact: John Quackenbush
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 3528
 Fax: 301 838 0208
 Email: johnq@tigr.org
 Plate: 277
 Seq primer: Forward.
 FEATURES Location/Qualifiers
 source 1..637
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone_lib="MAGE resequences, MAGK"
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ORIGIN

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Definition tigr-gss-dog-17000366002738 Dog Library Canis lupus familiaris
genomic, genomic survey sequence.
Accession CE539857
Version CE539857.1 GI:36856638
Keywords GSS.
Source Canis lupus familiaris (dog)
Organism Canis lupus familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae;
Canis.
Reference 1 (bases 1 to 429)
Authors Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
Title The dog genome: survey sequencing and comparative analysis
Journal Science 301 (5641), 1898-1903 (2003)
Pubmed 14512627
Comment Contact: Kirkness EF
The Institute for Genomic Research

Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES Location/Qualifiers

source

Location/Qualifiers

1. . . 429

/organism="Canis lupus familiaris"

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/strain="Standard Poodle"

/sub specie

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peripheral blood"

peripheral blood

ORIGIN

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Matches 144; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

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    77 GATGCCCTCGCCAACCACCTGCACTAACCTGCTGGTCTGAGACTGAGCCACTTGGAAAG 136
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    252 GAGGCTTAATGCTAACACCAGCATCAGTTGCCAACACTGGGAGTGAGCTCTCTGGAAA 193

    137 CTGATCTGGAGCACCAAGTCAGGCCCTAGCTGGCTGCAGCCACAGCCAACAAGACT 196
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    197 GCAACCTCCTGGGGATCCTGAGCCAGAACATCCCTGGCTAAATTGCT 243
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Job time : 1892 secs